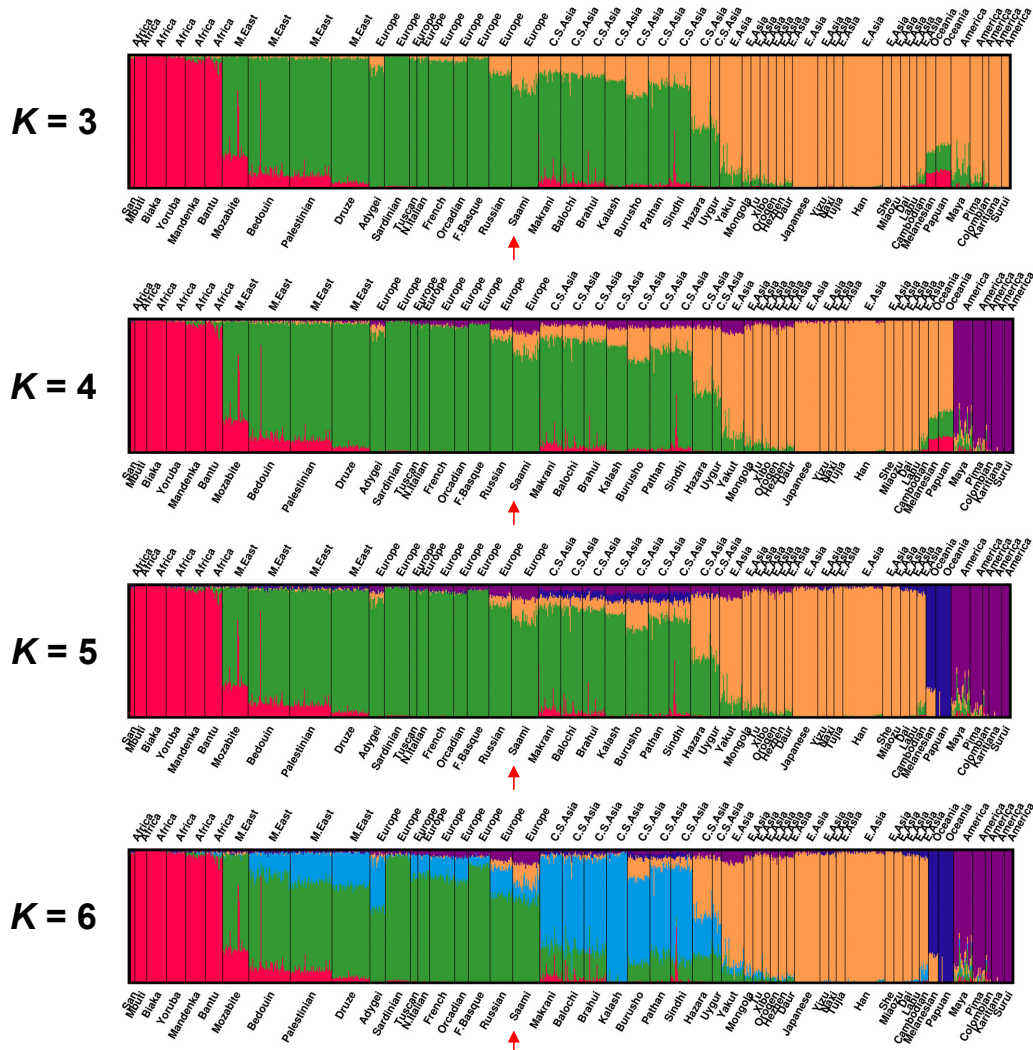


## Supplemental Data

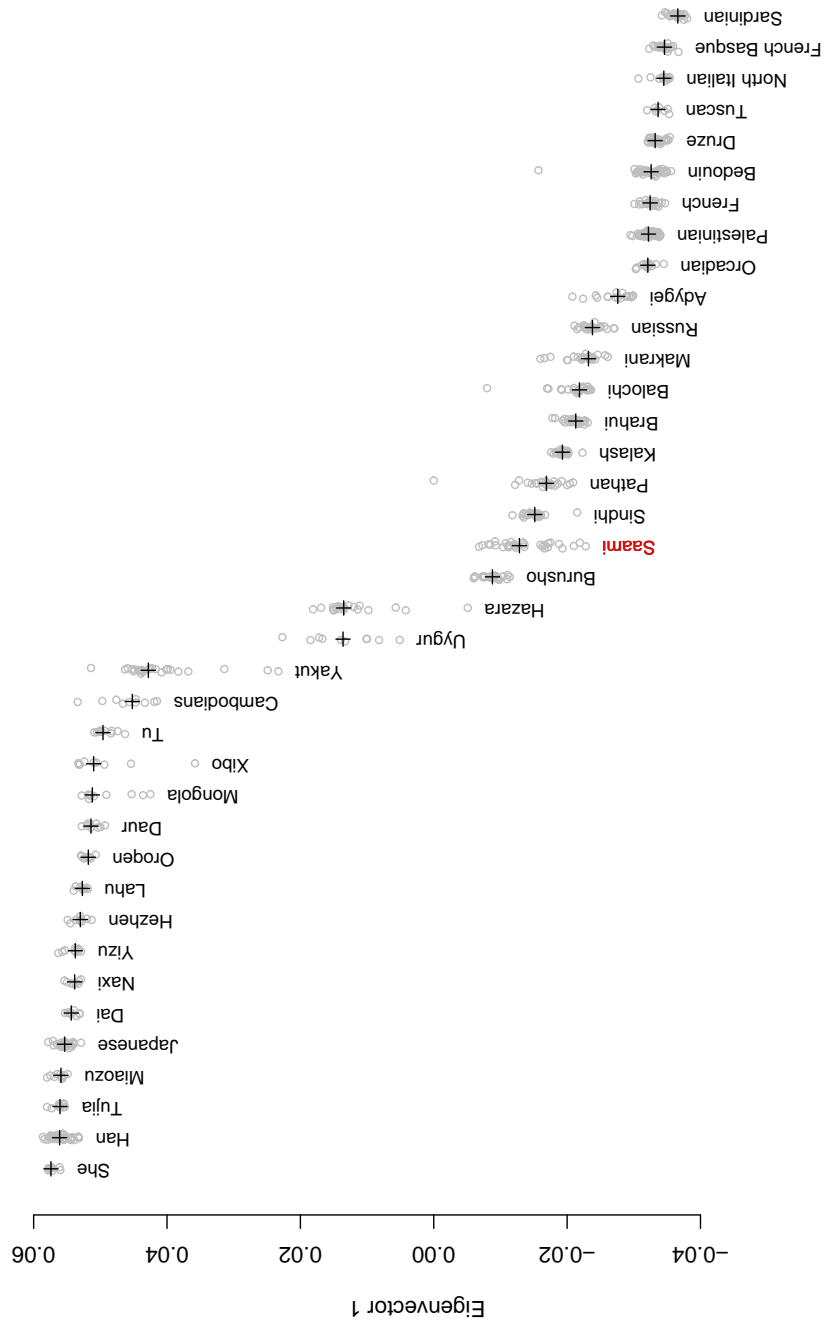
### **A genome-wide analysis of population structure in the Finnish Saami with implications for genetic association studies**

Jeroen R Huyghe, Erik Fransen, Samuli Hannula, Lut Van Laer, Els Van Eyken, Elina Mäki-Torkko, Pekka Aikio, Martti Sorri, Matthew J Huentelman, and Guy Van Camp



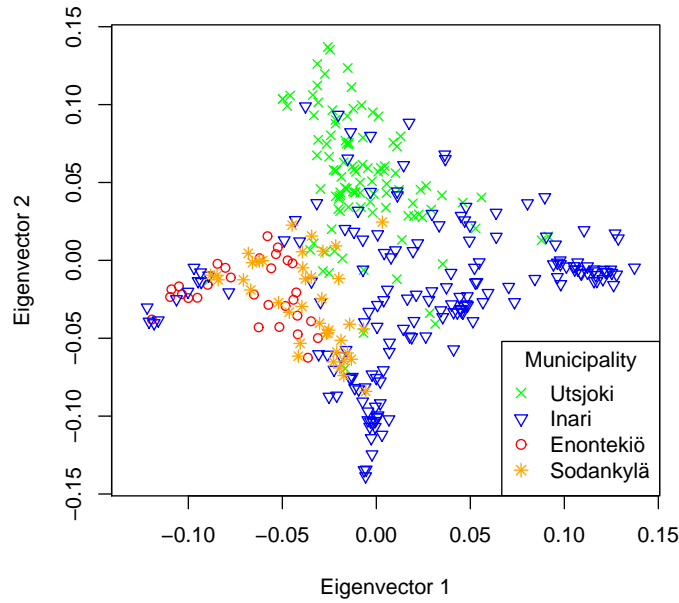
**Supplementary Figure 1: Model-based ancestry analysis based on the HGDP-CEPH data for  $K = 3$  to  $K = 6$**

Using the merged data on 37 931 autosomal SNPs for 30 unrelated Saami and for subjects from the HGDP project, ancestry for each individual was inferred with ADMIXTURE<sup>22</sup> at  $K = 3$  to  $K = 6$  and visualized with DISTRUCT.<sup>23</sup> Population labels were not used in this analysis. Ancestry components are color labeled by geographic region of origin following Li *et al.*<sup>7</sup>

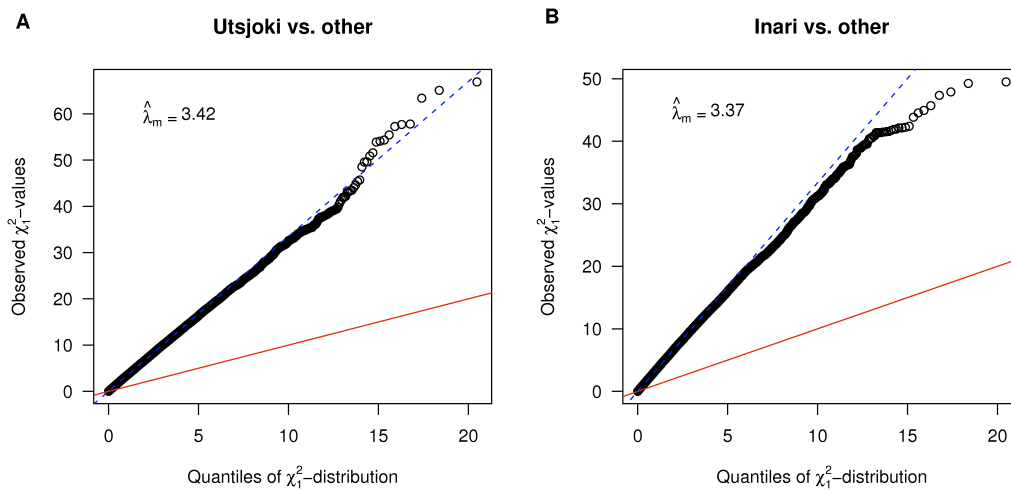


**Supplementary Figure 2: Jitter plot of the first eigenvector defined by the subset of HGDP-CEPH populations from Eurasia and the Middle East**

Projections for Saami were obtained as described in the legend of Figure 3. Crosses are population medians.



**Supplementary Figure 3: Hidden population structure within the Saami**  
 Scatter plot of the first two eigenvectors from the EIGENSOFT<sup>24</sup> analysis based on 344 Saami samples and 109 635 autosomal SNPs. Subjects are color labeled by municipality. Information on municipality was not used for the calculations.



**Supplementary Figure 4: Confounding in association studies due to population stratification and unaccounted relatedness**

Quantile-quantile plots showing the joint impact of population stratification and unaccounted relatedness on association mapping studies. Test statistics are from allele frequencies comparisons under worst case scenarios in which one municipality was compared with the others. Based on 82 914 SNPs with MAF > 5% and HWE P-value > 0.001. The dashed line goes through the first and third quartiles. Under the null hypothesis, the distribution is expected to fall close to the red line.